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RAW SEQUENCE LISTING

DATE: 10/07/2002

PATENT APPLICATION: US/09/978,318B

TIME: 14:11:19

Input Set : A:\EP.txt

Output Set: N:\CRF4\10072002\I978318B.raw

3 <110> APPLICANT: ALDAZ, MARCELO C.
 4 BEDNAREK, ANDRZEJ
 6 <120> TITLE OF INVENTION: WWOX: A PUTATIVE TUMOR SUPPRESSOR GENE MUTATED IN
 7 MULTIPLE CANCERS
 9 <130> FILE REFERENCE: UTSC:671US
 11 <140> CURRENT APPLICATION NUMBER: 09/978,318B
 12 <141> CURRENT FILING DATE: 2001-10-15
 14 <150> PRIOR APPLICATION NUMBER: 60/240,277
 15 <151> PRIOR FILING DATE: 2000-10-13
 17 <160> NUMBER OF SEQ ID NOS: 68
 19 <170> SOFTWARE: PatentIn Ver. 2.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 414
 23 <212> TYPE: PRT
 24 <213> ORGANISM: Human
 26 <400> SEQUENCE: 1
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 28 1 5 10 15
 30 Glu Leu Pro Pro Gly Trp Glu Glu Arg Thr Thr Lys Asp Gly Trp Val
 31 20 25 30
 33 Tyr Tyr Ala Asn His Thr Glu Glu Lys Thr Gln Trp Glu His Pro Lys
 34 35 40 45
 36 Thr Gly Lys Arg Lys Arg Val Ala Gly Asp Leu Pro Tyr Gly Trp Glu
 37 50 55 60
 39 Gln Glu Thr Asp Glu Asn Gly Gln Val Phe Phe Val Asp His Ile Asn
 40 65 70 75 80
 42 Lys Arg Thr Thr Tyr Leu Asp Pro Arg Leu Ala Phe Thr Val Asp Asp
 43 85 90 95
 45 Asn Pro Thr Lys Pro Thr Thr Arg Gln Arg Tyr Asp Gly Ser Thr Thr
 46 100 105 110
 48 Ala Met Glu Ile Leu Gln Gly Arg Asp Phe Thr Gly Lys Val Val Val
 49 115 120 125
 51 Val Thr Gly Ala Asn Ser Gly Ile Gly Phe Glu Thr Ala Lys Ser Phe
 52 130 135 140
 54 Ala Leu His Gly Ala His Val Ile Leu Ala Cys Arg Asn Met Ala Arg
 55 145 150 155 160
 57 Ala Ser Glu Ala Val Ser Arg Ile Leu Glu Glu Trp His Lys Ala Lys
 58 165 170 175
 60 Val Glu Ala Met Thr Leu Asp Leu Ala Leu Leu Arg Ser Val Gln His
 61 180 185 190
 63 Phe Ala Glu Ala Phe Lys Ala Lys Asn Val Pro Leu His Val Leu Val
 64 195 200 205
 66 Cys Asn Ala Ala Thr Phe Ala Leu Pro Trp Ser Leu Thr Lys Asp Gly

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69 Leu Glu Thr Thr Phe Gln Val Asn His Leu Gly His Phe Tyr Leu Val
70 225      230      235      240
72 Gln Leu Leu Gln Asp Val Leu Cys Arg Ser Ala Pro Ala Arg Val Ile
73      245      250      255
75 Val Val Ser Ser Glu Ser His Arg Phe Thr Asp Ile Asn Asp Ser Leu
76      260      265      270
78 Gly Lys Leu Asp Phe Ser Arg Leu Ser Pro Thr Lys Asn Asp Tyr Trp
79      275      280      285
81 Ala Met Leu Ala Tyr Asn Arg Ser Lys Leu Cys Asn Ile Leu Phe Ser
82      290      295      300
84 Asn Glu Leu His Arg Arg Leu Ser Pro Arg Gly Val Thr Ser Asn Ala
85 305      310      315      320
87 Val His Pro Gly Asn Met Met Tyr Ser Asn Ile His Arg Ser Trp Trp
88      325      330      335
90 Val Tyr Thr Leu Leu Phe Thr Leu Ala Arg Pro Phe Thr Lys Ser Met
91      340      345      350
93 Gln Gln Gly Ala Ala Thr Thr Val Tyr Cys Ala Ala Val Pro Glu Leu
94      355      360      365
96 Glu Gly Leu Gly Gly Met Tyr Phe Asn Asn Cys Cys Arg Cys Met Pro
97      370      375      380
99 Ser Pro Glu Ala Gln Ser Glu Glu Thr Ala Arg Thr Leu Trp Ala Leu
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103      405      410
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107 <211> LENGTH: 2264
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114 cagccatggc agcgtgcgc tacgcggggc tggacgacac ggacagtga gacgagctgc 180
115 ctccgggctg ggaggagaga accaccaag acggctgggt ttactacgcc aatcacaccg 240
116 aggagaagac tcagtgggaa catccaaaaa ctggaaaaaag aaaacgagtg gcaggagatt 300
117 tgccatacgg atgggaacaa gaaactgat agaacggaca agtggttttt gttgaccata 360
118 taaataaaaag aaccacctac ttggaccaa gactggcggt tactgtggat gataatccga 420
119 ccaagccaac caccggcaa agatacgacg gcagcaccac tgccatggaa attctccagg 480
120 gccgggattt cactggcaaa gtggttggtg tcaactggagc taattcagga atagggttcg 540
121 aaaccgccaa gtcttttgcc ctccatggtg cacatgtgat cttggcctgc aggaacatgg 600
122 caagggcgag tgaagcagtg tcacgcattt tagaagaatg gcataaagcc aaggtagaag 660
123 caatgacctt ggacctcgct ctgctccgta gcgtgcagca ttttgetgaa gcattcaagg 720
124 ccaagaatgt gcctcttcat gtgcttggtg gcaacgcagc aacttttgct ctaccttgga 780
125 gtctcaccaa agatggcctg gagaccacct ttcaagtga tcatctgggg cacttctacc 840
126 ttgtccagct cctccaggat gttttgtgcc gctcagctcc tgcccgtgtc attgtggtct 900
127 cctcagagtc ccatcgattt acagatatta acgactcctt gggaaaactg gacttcagtc 960
128 gcctctctcc aacaaaaaac gactattggg cgatgctggc ttataacagg tccaagctct 1020
129 gcaacatcct cttctccaac gagctgcacc gtcgcctctc cccacgcggg gtcacgtcga 1080
130 acgcagtga tcctggaaat atgatgtact ccaacattca tcgcagctgg tgggtgtaca 1140

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131 cactgctgtt taccttggcg aggcctttca ccaagtccat gcaacaggga gctgccacca 1200
132 cegtgtactg tgctgctgtc ccagaactgg agggctctggg agggatgtac ttcaacaact 1260
133 gctgcoctg catgccctca ccagaagctc agagcgaaga gacggcccgg accctgtggg 1320
134 cgctcagcga gaggctgata caagaacggc ttggcagcca gtccggctaa gtggagctca 1380
135 gagcggatgg gcacacacac ccgccctgtg tgtgtccctt cacgcaagtg ccagggtgg 1440
136 gcccttcca aatgtccctc caacacagat ccgcaagagt aaaggaaata agagcagtca 1500
137 caacagagtg aaaaatctta agtaccatg ggaagcaggg aattcctggg gtaaagtatc 1560
138 actttttctg ggtctgggcta ggcataggtc tctttgcttt ctggtggtgg cctgtttgaa 1620
139 agtaaaaacc tgcttgggtg gtaggttccg tatctccctg gagaagcacc agcaattctc 1680
140 tttcttttac tgttatagaa tagcctgagg tcccctcgtc ccatccagct accaccacgg 1740
141 ccaccactgc agccgggggc tggccttctc ctacttaggg aagaaaaagc aagtgttcac 1800
142 tgctccttgc tgcattgatc caggagataa ttgtttcatt catcctgacc aagactgagc 1860
143 cagcttagca actgctgggg agacaaatct cagaacctg tcccagccag tgaggatgac 1920
144 agtgacaccc agagggagta gaatacgag aactaccagg tggcaaagta cttgtcatag 1980
145 actcctttgc taatgctatg caaaaaattc tttagagatt ataacaaatt tttcaaatca 2040
146 ttccttagat accttgaaag gcaggaaggg aagcgtatat acttaagaat acacaggata 2100
147 ttttgggggg cagagaataa aacgttagtt aatcccttg tctgtcaatc acagtctcag 2160
148 ttctcttgct ttcacattgt acttaaacct cctgctgtgc ctgcctcct atgcttaata 2220
149 aaagaacatg cttgaatatc aaaaaaaaaa aaaaaaaaaa aaaa 2264
152 <210> SEQ ID NO: 3
153 <211> LENGTH: 26
154 <212> TYPE: DNA
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157 <400> SEQUENCE: 3
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161 <210> SEQ ID NO: 4
162 <211> LENGTH: 29
163 <212> TYPE: DNA
164 <213> ORGANISM: Homo sapiens
166 <400> SEQUENCE: 4
167 acggtggtgg cagctccctg ttgcgatg 29
170 <210> SEQ ID NO: 5
171 <211> LENGTH: 33
172 <212> TYPE: DNA
173 <213> ORGANISM: Homo sapiens
175 <400> SEQUENCE: 5
176 acggtggtgg cagctccctg ttgacattct tgg 33
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180 <211> LENGTH: 32
181 <212> TYPE: DNA
182 <213> ORGANISM: Homo sapiens
184 <400> SEQUENCE: 6
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188 <210> SEQ ID NO: 7
189 <211> LENGTH: 30
190 <212> TYPE: DNA
191 <213> ORGANISM: Homo sapiens
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194 acggtggtgg cagctccctg ttgctattcc 30

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197 <210> SEQ ID NO: 8
198 <211> LENGTH: 33
199 <212> TYPE: DNA
200 <213> ORGANISM: Homo sapiens
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207 <211> LENGTH: 27
208 <212> TYPE: DNA
209 <213> ORGANISM: Homo sapiens
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212 acggtggtgg cagctccctg ttgctcc 27
215 <210> SEQ ID NO: 10
216 <211> LENGTH: 19
217 <212> TYPE: DNA
218 <213> ORGANISM: Homo sapiens
220 <400> SEQUENCE: 10
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224 <210> SEQ ID NO: 11
225 <211> LENGTH: 21
226 <212> TYPE: DNA
227 <213> ORGANISM: Homo sapiens
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230 agctccctgt tgcattgact t 21
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234 <211> LENGTH: 22
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252 <211> LENGTH: 21
253 <212> TYPE: DNA
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256 <400> SEQUENCE: 14
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261 <211> LENGTH: 22
262 <212> TYPE: DNA
263 <213> ORGANISM: Homo sapiens
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266 cagccctggc acttgctga gg 22
269 <210> SEQ ID NO: 16

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270 <211> LENGTH: 22
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278 <210> SEQ ID NO: 17
279 <211> LENGTH: 23
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281 <213> ORGANISM: Homo sapiens
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288 <211> LENGTH: 30
289 <212> TYPE: DNA
290 <213> ORGANISM: Homo sapiens
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297 <211> LENGTH: 22
298 <212> TYPE: DNA
299 <213> ORGANISM: Homo sapiens
301 <400> SEQUENCE: 19
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305 <210> SEQ ID NO: 20
306 <211> LENGTH: 30
307 <212> TYPE: DNA
308 <213> ORGANISM: Homo sapiens
310 <400> SEQUENCE: 20
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314 <210> SEQ ID NO: 21
315 <211> LENGTH: 20
316 <212> TYPE: DNA
317 <213> ORGANISM: Homo sapiens
319 <220> FEATURE:
320 <221> NAME/KEY: modified_base
321 <222> LOCATION: (3)..(5)
322 <223> OTHER INFORMATION: R = A OR G
324 <400> SEQUENCE: 21
325 cccrcaata ctacatccta                    20
328 <210> SEQ ID NO: 22
329 <211> LENGTH: 20
330 <212> TYPE: DNA
331 <213> ORGANISM: Homo sapiens
333 <220> FEATURE:
334 <221> NAME/KEY: modified_base
335 <222> LOCATION: (11)
336 <223> OTHER INFORMATION: Y = C OR T/U
338 <400> SEQUENCE: 22
339 gggatgaggt ygttttggtt                  20

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VERIFICATION SUMMARY

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L:678 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32

L:1066 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1